

TECH CENTER 1600/2900

NOV 15 2001

#6 RECEIVED  
1642

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/619,310

DATE: 11/05/2001

TIME: 13:21:01

Input Set : A:\2001-09-28 seqlist.ST25.txt

Output Set: N:\CRF3\11022001\I619310.raw

5 <110> APPLICANT: BioImage A/S  
 7 Thastrup, Ole  
 11 <120> TITLE OF INVENTION: Novel Florescent Proteins  
 15 <130> FILE REFERENCE: 3759-0106P  
 C--> 19 <140> CURRENT APPLICATION NUMBER: US/09/619,310 *OK*  
 C--> 21 <141> CURRENT FILING DATE: 2000-07-19

25 <160> NUMBER OF SEQ ID NOS: 8  
 29 <170> SOFTWARE: PatentIn version 3.1  
 33 <210> SEQ ID NO: 1

35 &lt;211&gt; LENGTH: 764

37 &lt;212&gt; TYPE: DNA

39 &lt;213&gt; ORGANISM: Aequorea victoria

43 &lt;220&gt; FEATURE:

45 &lt;221&gt; NAME/KEY: CDS

47 &lt;222&gt; LOCATION: (8)..(721)

49 &lt;223&gt; OTHER INFORMATION:

53 &lt;400&gt; SEQUENCE: 1.

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55		Met	Ser	Lys	Gly	Glu	Glu	Leu	Phe	Thr	Gly	Val	Val	Pro	Ile	
56		1			5						10					
58	ctt	gtt	gaa	tta	gat	ggc	gat	gtt	aat	ggg	caa	aaa	ttc	tct	gtt	agt
59	Leu	Val	Glu	Leu	Asp	Gly	Asp	Val	Asn	Gly	Gln	Lys	Phe	Ser	Val	Ser
60	15				20					25					30	
62	gga	gag	ggt	gaa	ggt	gat	gca	aca	tac	gga	aaa	ctt	acc	ctt	aaa	ttt
63	Gly	Glu	Gly	Glu	Gly	Asp	Ala	Thr	Tyr	Gly	Lys	Leu	Thr	Leu	Lys	Phe
64					35					40					45	
66	att	tgc	act	act	ggg	aag	cta	cct	gtt	cca	tgg	cca	acg	ctt	gtc	act
67	Ile	Cys	Thr	Thr	Gly	Lys	Leu	Pro	Val	Pro	Trp	Pro	Thr	Leu	Val	Thr
68					50				55					60		
70	act	ttc	tct	tat	ggt	gtt	caa	tgc	ttt	tca	aga	tac	cca	gat	cat	atg
71	Thr	Phe	Ser	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met
72					65				70				75			
74	aaa	cag	cat	gac	ttt	ttc	aag	agt	gcc	atg	ccc	gaa	ggt	tat	gta	cag
75	Lys	Gln	His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln
76		80					85				90					
78	gaa	aga	act	ata	ttt	tac	aaa	gat	gac	ggg	aac	tac	aag	aca	cgt	gct
79	Glu	Arg	Thr	Ile	Phe	Tyr	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala
80	95				100					105				110		
82	gaa	gtc	aag	ttt	gaa	ggt	gat	acc	ctt	gtt	aat	aga	atc	gag	tta	aaa
83	Glu	Val	Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys
84					115					120				125		
86	ggt	att	gat	ttt	aaa	gaa	gat	gga	aac	att	ctt	gga	cac	aaa	atg	gaa
87	Gly	Ile	Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Met	Glu
88					130				135					140		
90	tac	aac	tat	aac	tca	cat	aat	gta	tac	atc	atg	gca	gac	aaa	cca	aag
91	Tyr	Asn	Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Pro	Lys
92					145				150					155		

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94 aat gga atc aaa gtt aac ttc aaa att aga cac aac att aaa gat gga      529
95 Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly
96      160      165      170
98 agc gtt caa tta gca gac cat tat caa caa aat act cca att ggc gat      577
99 Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
100 175      180      185      190
102 ggc cct gtc ctt tta cca gac aac cat tac ctg tcc acg caa tct gcc      625
103 Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala
104      195      200      205
106 ctt tcc aaa gat ccc aac gaa aag aga gat cac atg atc ctt ctt gag      673
107 Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu
108      210      215      220
110 ttt gta aca gct gct ggg att aca cat ggc atg gat gaa cta tac aaa      721
111 Phe Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
112      225      230      235
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117 <210> SEQ ID NO: 2
119 <211> LENGTH: 238
121 <212> TYPE: PRT
123 <213> ORGANISM: Aequorea victoria
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133 Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser Gly Glu
134      20      25      30
137 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
138      35      40      45
141 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
142      50      55      60
145 Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
146 65      70      75      80
149 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
150      85      90      95
153 Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
154      100      105      110
157 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
158      115      120      125
161 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu Tyr Asn
162      130      135      140
165 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys Asn Gly
166 145      150      155      160
169 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly Ser Val
170      165      170      175
173 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
174      180      185      190
177 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
178      195      200      205
181 Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu Phe Val
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186 225                               230                               235
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191 <211> LENGTH: 757
193 <212> TYPE: DNA
195 <213> ORGANISM: Aequorea victoria
199 <220> FEATURE:
201 <221> NAME/KEY: CDS
203 <222> LOCATION: (1)..(717)
205 <223> OTHER INFORMATION:
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212 1                               5                               10                               15
214 gaa tta gat ggc gat gtt aat ggg caa aaa ttc tcc gtt agt gga gag      96
215 Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser Gly Glu
216                               20                               25                               30
218 ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa ttt att tgc      144
219 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
220                               35                               40                               45
222 act act ggg aag cta cct gtt cca tgg cca acg ctt gtc act act ctc      192
223 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
224                               50                               55                               60
226 tct cat ggt gtt caa tgc ttt tct aga tac cca gat cat atg aaa cag      240
227 Ser His Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
228 65'                               70                               75                               80
230 cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa aga      288
231 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
232                               85                               90                               95
234 act ata ttt tac aaa gat gac ggg aac tac aag aca cgt gct gaa gtc      336
235 Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
236                               100                              105                              110
238 aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt att      384
239 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
240                               115                              120                              125
242 gat ttt aaa gaa gat gga aac att ctt gga cac aaa atg gaa tac aat      432
243 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu Tyr Asn
244                               130                              135                              140
246 tat aac tca cat aat gta tac atc atg gca gac aaa cca aag aat ggc      480
247 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys Asn Gly
248 145                               150                               155                               160
250 atc aaa gtt aac ttc aaa att aga cac aac att aaa gat gga agc gtt      528
251 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly Ser Val
252                               165                              170                              175
254 caa tta gca gac cat tat caa caa aat act cca att ggc gat ggc cct      576
255 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
256                               180                              185                              190
258 gtc ctt tta cca gac aac cat tac ctg tcc acg caa tct gcc ctt tcc      624
259 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser

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260          195          200          205
262 aaa gat ccc aac gaa aag aga gat cac atg atc ctt ctt gag ttt gta      672
263 Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu Phe Val
264          210          215          220
266 aca gct gct ggg att aca cat ggc atg gat gaa cta tac aaa taa      717
267 Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
268 225          230          235
270 atgtccagac ttccaattga cactaaaggg atccgaattc      757
273 <210> SEQ ID NO: 4
275 <211> LENGTH: 238
277 <212> TYPE: PRT
279 <213> ORGANISM: Aequorea victoria
283 <400> SEQUENCE: 4
285 Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
286 1          5          10          15
289 Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser Gly Glu
290          20          25          30
293 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
294          35          40          45
297 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
298          50          55          60
301 Ser His Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
302 65          70          75          80
305 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
306          85          90          95
309 Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
310          100          105          110
313 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
314          115          120          125
317 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu Tyr Asn
318          130          135          140
321 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys Asn Gly
322 145          150          155          160
325 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys Asp Gly Ser Val
326          165          170          175
329 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
330          180          185          190
333 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
334          195          200          205
337 Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu Leu Glu Phe Val
338          210          215          220
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342 225          230          235
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347 <211> LENGTH: 817
349 <212> TYPE: DNA
351 <213> ORGANISM: Aequorea victoria
355 <220> FEATURE:
357 <221> NAME/KEY: CDS

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Output Set: N:\CRF3\11022001\I619310.raw

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359 <222> LOCATION: (1)..(777)
361 <223> OTHER INFORMATION:
365 <400> SEQUENCE: 5
366 atg agt aaa gga gaa gaa ctt ttc act gga gtt gtc cca att ctt gtt      48
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368 1          5          10          15
370 gaa tta gat ggc gat gtt aat ggg caa aaa ttc tct gtt agt gga gag      96
371 Glu Leu Asp Gly Asp Val Asn Gly Gln Lys Phe Ser Val Ser Gly Glu
372          20          25          30
374 ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa ttt att tgc      144
375 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
376          35          40          45
378 act act ggg aag cta cct gtt cca tgg cca acg ctt gtc act act ctc      192
379 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu
380          50          55          60
382 tct tat ggt gtt caa tgc ttt tct aga tac cca gat cat atg aaa cag      240
383 Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
384 65          70          75          80
386 cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa aga      288
387 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
388          85          90          95
390 act ata ttt tac aaa gat gac ggg aac tac aag aca cgt gct gaa gtc      336
391 Thr Ile Phe Tyr Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
392          100          105          110
394 aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt att      384
395 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
396          115          120          125
398 gat ttt aaa gaa gat gga aac att ctt gga cac aaa atg gaa tac aat      432
399 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Met Glu Tyr Asn
400          130          135          140
402 tat aac tca cat aat gta tac atc atg gca gac aaa cca aag aat ggc      480
403 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Pro Lys Asn Gly
404 145          150          155          160
406 atg gaa tac aat tat aac tca cat aat gta tac atc atg gca gac aaa      528
407 Met Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys
408          165          170          175
410 cca aag aat ggc atc aaa gtt aac ttc aaa att aga cac aac att aaa      576
411 Pro Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Lys
412          180          185          190
414 gat gga agc gtt caa tta gca gac cat tat caa caa aat act cca att      624
415 Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
416          195          200          205
418 ggc gat ggc cct gtc ctt tta cca gac aac cat tac ctg tcc acg caa      672
419 Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln
420          210          215          220
422 tct gcc ctt tcc aaa gat ccc aac gaa aag aga gat cac atg atc ctt      720
423 Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Ile Leu
424 225          230          235          240
426 ctt gag ttt gta aca gct gct ggg att aca cat ggc atg gat gaa cta      768

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VERIFICATION SUMMARY

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Input Set : A:\2001-09-28 seqlist.ST25.txt

Output Set: N:\CRF3\11022001\I619310.raw

L:19 M:270 C: Current Application Number differs, Replaced Current Application Number

L:21 M:271 C: Current Filing Date differs, Replaced Current Filing Date